RAW SEQUENCE LISTING

EFS

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Application Serial Number: _10/511,813_
Source: _1Fw16_
Date Processed by STIC: _3/15/07_

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RAW SEQUENCE LISTING   DATE: 03/15/2007
PATENT APPLICATION: US/10/511,813   TIME: 14:38:29

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Output Set: N:\CRF4\03152007\J511813.raw

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 3 <110> APPLICANT: COY, Johannes
 5 <120> TITLE OF INVENTION: Compositions and methods for detection and treatment of
 6       proliferative abnormalities associated with overexpression of
 7       human transketolase like-1 gene
 9 <130> FILE REFERENCE: 4007-008
11 <140> CURRENT APPLICATION NUMBER: 10/511,813
12 <141> CURRENT FILING DATE: 2004-10-19
14 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03827
15 <151> PRIOR FILING DATE: 2003-04-12
17 <150> PRIOR APPLICATION NUMBER: EP 02008831.6
18 <151> PRIOR FILING DATE: 2002-04-19
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn version 3.4
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2531
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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34 gcaccttgca ggtgttgcaa gatatggcca gccgcttgcg aatccattcc atcagggcca     180
36 catgctccac gagctccggc caccctacat catgtagcag ttcttctgag atcatgtctg     240
38 tgctgttctt ctacatcatg aggtacaagc agtcagatcc agagaatccg gacaacgacc     300
40 gatttgtcct cgcaaagaga ctgtcgtttg tggatgtggc aacaggatgg ctcggacaag     360
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52 tctggcaggc ttctcaggtg aagcacaagc ccactgctgt ggtggccaag accttcaagg     720
54 gccggggcac cccaagtatt gaggatgcag aaagttggca tgcaaagcca atgccgagag     780
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 92 gctgttagcc ttggtctttt ggcctcttta ccctgtgttt atgtttgttc caaaaccatc  1920
 94 atttaaatct ctactgtcac attttgtttc ttaaaagcaa agccagctaa caccttcatt  1980
 96 catccctagt tcggaaattc aagctaacta cttacccttt aaactgtcac tgcatatgca  2040
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100 aggtaacaaa acaaccacct gatagtaagt tttctgataa gactatagat aagtggtaga  2160
102 ggtaatcaat tcttccgaag tgtttccttc gtgaataact ggtagaggta atagtttttt  2220
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110 cacgtttgag aggctgtcag gcagcagcga aagcttgtta ggatgtcctg tgctgcttgt  2460
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132 Ile His Ser Ile Arg Ala Thr Cys Ser Thr Ser Ser Gly His Pro Thr
133             35                  40                  45
136 Ser Cys Ser Ser Ser Ser Glu Ile Met Ser Val Leu Phe Phe Tyr Ile
137         50                  55                  60
140 Met Arg Tyr Lys Gln Ser Asp Pro Glu Asn Pro Asp Asn Asp Arg Phe
141 65                  70                  75                  80
144 Val Leu Ala Lys Arg Leu Ser Phe Val Asp Val Ala Thr Gly Trp Leu
145                 85                  90                  95
148 Gly Gln Gly Leu Gly Val Ala Cys Gly Met Ala Tyr Thr Gly Lys Tyr
149                 100                 105                 110
152 Phe Asp Arg Ala Ser Tyr Arg Val Phe Cys Leu Met Ser Asp Gly Glu
153             115                 120                 125
156 Ser Ser Glu Gly Ser Val Trp Glu Ala Met Ala Phe Ala Ser Tyr Tyr
157         130                 135                 140
160 Ser Leu Asp Asn Leu Val Ala Ile Phe Asp Val Asn Arg Leu Gly His
161 145                 150                 155                 160
164 Ser Gly Ala Leu Pro Ala Glu His Cys Ile Asn Ile Tyr Gln Arg Arg
165                 165                 170                 175
168 Cys Glu Ala Phe Gly Trp Asn Thr Tyr Val Val Asp Gly Arg Asp Val
169             180                 185                 190
172 Glu Ala Leu Cys Gln Val Phe Trp Gln Ala Ser Gln Val Lys His Lys
173         195                 200                 205
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177     210                 215             220
180 Ile Glu Asp Ala Glu Ser Trp His Ala Lys Pro Met Pro Arg Glu Arg
181 225             230             235                 240
184 Ala Asp Ala Ile Ile Lys Leu Ile Glu Ser Gln Ile Gln Thr Ser Arg
185             245             250                 255
188 Asn Leu Asp Pro Gln Pro Pro Ile Glu Asp Ser Pro Glu Val Asn Ile
189         260             265             270
192 Thr Asp Val Arg Met Thr Ser Pro Pro Asp Tyr Arg Val Gly Asp Lys
193         275             280             285
196 Ile Ala Thr Arg Lys Ala Cys Gly Leu Ala Leu Ala Lys Leu Gly Tyr
197     290             295             300
200 Ala Asn Asn Arg Val Val Val Leu Asp Gly Asp Thr Arg Tyr Ser Thr
201 305             310             315             320
204 Phe Ser Glu Ile Phe Asn Lys Glu Tyr Pro Glu Arg Phe Ile Glu Cys
205             325             330             335
208 Phe Met Ala Glu Gln Asn Met Val Ser Val Ala Leu Gly Cys Ala Ser
209             340             345             350
212 Arg Gly Arg Thr Ile Ala Phe Ala Ser Thr Phe Ala Ala Phe Leu Thr
213     355             360             365
216 Arg Ala Phe Asp His Ile Arg Ile Gly Gly Leu Ala Glu Ser Asn Ile
217     370             375             380
220 Asn Ile Ile Gly Ser His Cys Gly Val Ser Val Gly Asp Asp Gly Ala
221 385             390             395             400
224 Ser Gln Met Ala Leu Glu Asp Ile Ala Met Phe Arg Thr Ile Pro Lys
225             405             410             415
228 Cys Thr Ile Phe Tyr Pro Thr Asp Ala Val Ser Thr Glu His Ala Val
229             420             425             430
232 Ala Leu Ala Ala Asn Ala Lys Gly Met Cys Phe Ile Arg Thr Thr Arg
233     435             440             445
236 Pro Glu Thr Met Val Ile Tyr Thr Pro Gln Glu Arg Phe Glu Ile Gly
237     450             455             460
240 Gln Ala Lys Val Leu Arg His Cys Val Ser Asp Lys Val Thr Val Ile
241 465             470             475             480
244 Gly Ala Gly Ile Thr Val Tyr Glu Ala Leu Ala Ala Ala Asp Glu Leu
245             485             490             495
248 Ser Lys Gln Asp Ile Phe Ile Arg Val Ile Asp Leu Phe Thr Ile Lys
249             500             505             510
252 Pro Leu Asp Val Ala Thr Ile Val Ser Ser Ala Lys Ala Thr Glu Gly
253         515             520             525
256 Arg Ile Ile Thr Val Glu Asp His Tyr Pro Gln Gly Gly Ile Gly Glu
257     530             535             540
260 Ala Val Cys Ala Ala Val Ser Met Asp Pro Asp Ile Gln Val His Ser
261 545             550             555             560
264 Leu Ala Val Ser Gly Val Pro Gln Ser Gly Lys Ser Glu Glu Leu Leu
265             565             570             575
268 Asp Met Tyr Gly Ile Ser Ala Arg His Ile Ile Val Ala Val Lys Cys
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279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 3
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287 Cys Glu Ala Phe Gly Trp Asn Thr Tyr Val Val Asp Gly Arg Asp Val
288         20                  25                  30
291 Glu Ala Leu Cys Gln Val Phe Trp Gln Ala Ser Gln Val Lys His Lys
292         35                  40                  45
295 Pro Thr Ala Val Val Ala Lys Thr Phe Lys Gly Arg Gly Thr Pro Ser
296     50                  55                  60
299 Ile Glu Asp Ala Glu Ser Trp His Ala Lys Pro Met Pro Arg Glu Arg
300 65                  70                  75                  80
303 Ala Asp Ala Ile Ile Lys Leu Ile Glu Ser Gln Ile Gln Thr Ser Arg
304             85                  90                  95
307 Asn Leu Asp Pro Gln Pro Pro Ile Glu Asp Ser Pro Glu Val Asn Ile
308             100                 105                 110
311 Thr Asp Val Arg Met Thr Ser Pro Pro Asp Tyr Arg Val Gly Asp Lys
312         115                 120                 125
315 Ile Ala Thr Arg Lys Ala Cys Gly Leu Ala Leu Ala Lys Leu Gly Tyr
316     130                 135                 140
319 Ala Asn Asn Arg Val Val Val Leu Asp Gly Asp Thr Arg Tyr Ser Thr
320 145                 150                 155                 160
323 Phe Ser Glu Ile Phe Asn Lys Glu Tyr Pro Glu Arg Phe Ile Glu Cys
324             165                 170                 175
327 Phe Met Ala Glu Gln Asn Met Val Ser Val Ala Leu Gly Cys Ala Ser
328         180                 185                 190
331 Arg Gly Arg Thr Ile Ala Phe Ala Ser Thr Phe Ala Ala Phe Leu Thr
332     195                 200                 205
335 Arg Ala Phe Asp His
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340 <211> LENGTH: 17
341 <212> TYPE: PRT
342 <213> ORGANISM: Homo sapiens
344 <400> SEQUENCE: 4
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355 <211> LENGTH: 15
356 <212> TYPE: PRT
357 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING

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375 <211> LENGTH: 20
376 <212> TYPE: DNA
377 <213> ORGANISM: Homo sapiens
379 <400> SEQUENCE: 7
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384 <211> LENGTH: 20
385 <212> TYPE: DNA
386 <213> ORGANISM: Homo sapiens
388 <400> SEQUENCE: 8
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393 <211> LENGTH: 20
394 <212> TYPE: DNA
395 <213> ORGANISM: Homo sapiens
397 <400> SEQUENCE: 9
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VERIFICATION SUMMARY

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